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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=2; day=5; hr=14; min=17; sec=45; ms=80; ]

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\*\*\*\*\*

Reviewer Comments:

<210> 7

<211> 54

<212> DNA

<213> Oligonucleotide Primer CF59

<400> 7

cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc

54

The above <213> response is invalid, also similar responses were found in sequence id#'s 10 and 11. FYI, these responses can be inserted into section <220> to <223>.

\*\*\*\*\*

Application No: 10584438 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2008-01-29 15:17:14.169  
**Finished:** 2008-01-29 15:17:15.923  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 754 ms  
**Total Warnings:** 20  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 20  
**Actual SeqID Count:** 20

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

**Input Set:**

**Output Set:**

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**Total Errors:** 1  
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**Actual SeqID Count:** 20

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

<210> 1  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Linker VC053

<400> 1  
gatctttgga taagagagac gctcacaagt ccgaagtgc tcaccggt 48

<210> 2  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Linker VC054

<400> 2  
ccttgaacct gtgagcgact tcggacttgt gagcgtctct cttatccaaa 50

<210> 3  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Linker VC055

<400> 3  
gatctttgga taagagagac gctcacaagt ccgaagtgc tcatcgat 48

<210> 4  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Linker VC056

<400> 4  
ccttgaatcg atgagcgact tcggacttgt gagcgtctct cttatccaaa 50

<210> 5  
<211> 86  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Linker VC057

<400> 5  
tcaaggaccc aggtgaggaa aacttcaagg ctttggctt gatcgcttc gctcaatact 60  
tgcaacaatg tccattcgaa gatcac 86

<210> 6

<211> 80  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Linker VC058

<400> 6  
gtgatcttcg aatggacatt gttgcaagta ttgagcgaaa gcgatcaaga ccaaagcctt 60  
gaagtttcc tcaccttaggt 80

<210> 7  
<211> 54  
<212> DNA  
<213> Oligonucleotide Primer CF59

<400> 7  
cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc 54

<210> 8  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide linker SEQ ID 8

<400> 8  
Gly Gly Gly Gly Ser  
1 5

<210> 9  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide linker SEQ ID 9

<400> 9  
Gly Gly Gly Ser  
1

<210> 10  
<211> 17  
<212> PRT  
<213> Stanniocalcin signal peptide sequence

<400> 10  
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser  
1 5 10 15

Ala

<210> 11  
<211> 22

<212> PRT  
<213> Consensus signal sequence

<400> 11  
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu  
1 5 10 15

Trp Ala Pro Ala Arg Gly  
20

<210> 12  
<211> 66  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Primer CF60

<400> 12  
ggccatcgat gagcgacttc ggacttgtga gcgtccagcc gagtcttcag cagcagcagt 60  
ccccctc 66

<210> 13  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Primer CF61

<400> 13  
ccggccttag gcttacctgg gccaccacct ggcccccctc gagtttcccc 50

<210> 14  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide Primer CF62

<400> 14  
ggccaagctt attacagccg agtcttcagc agcagcagtc ccctc 45

<210> 15  
<211> 2358  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> N-terminal IL11-albumin fusion

<400> 15  
atgaagtggg ttttcatcggt ctccattttg ttcttggttct cctctgctta ctcttagatct 60  
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ctggacagaca ccgtgctctt gacccgctctt ctccctggcgg acacgcggca gctggctgca 180  
cagctgaggc acaaattccc agctgacggg gaccacaacc tgattccctt gcccacccctg 240

ccatggatcg cgggggcaact gggagctcta cagctcccag gtgtgctgac aaggctgcga  
gcggacacct tgccttaccc gcggcacgtg cagtggtcgc gcccggcagg tggcttcc  
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cggtgcgc cccctgcggc tcctgatgtc ccgcctggcc ctgccccagc caccggcgggaa  
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ctggacgctc acaagtcccgaa agtcgctcat cgattcaagg accttaggtga ggaaaacttc  
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aatgtttct tgcaacacaa ggacgacaac ccaaacttgc caagattgggtagaccagaa  
gttgcgtca tgcgtactgc ttccacgc aacgaagaaaa cttcttgaa gaagtacttg  
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aaggttcaca ctgaatgttg tcaacggtgcac ttgttggaaat gtgctgtatc cagagctgac  
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gaatacaagt tccaaaacgc ttgttgggtt agataacta aagggatccc acaagtctcc  
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<210>	16
<211>	786
<212>	PRT
<213>	Artificial Sequence

<220>  
<223> N-terminal III-1-albumin fusion

<400> 16  
Met Lys Trp Val Phe Ile Val Ser Ile Leu Phe Leu Phe Ser Ser Ala  
1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg Gly Pro Pro Pro Gly Pro Pro Arg  
                  20                 25                                 30

Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr  
35 40 45

Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp  
50 55 60

Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu  
65 70 75 80

Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu  
85 90 95

Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp  
100 105 110

Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu  
115 120 125

Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu  
130 135 140

Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala  
145 150 155 160

Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala  
165 170 175

His Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg  
180 185 190

Gly Leu Leu Leu Leu Lys Thr Arg Leu Asp Ala His Lys Ser Glu Val  
195 200 205

Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val  
210 215 220

Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His  
225 230 235 240

Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala  
245 250 255

Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly  
260 265 270

Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met  
275 280 285

Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu  
290 295 300

Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu  
305 310 315 320

Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu  
325 330 335

Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala  
340 345 350

Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu  
355 360 365

Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp  
370 375 380

Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys  
385 390 395 400

Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala  
405 410 415

Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val  
420 425 430

Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His  
435 440 445

Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr  
450 455 460

Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys  
465 470 475 480

Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn  
485 490 495

Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu  
500 505 510

Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu  
515 520 525

Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val  
530 535 540

Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys  
545 550 555 560

Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp  
565 570 575

Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn  
580 585 590

Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu  
595 600 605

Leu Val Arg Tyr Thr Lys Val Pro Gln Val Ser Thr Pro Thr Leu  
610 615 620

Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys  
625 630 635 640

His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val  
645 650 655

Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp  
660 665 670

Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys  
675 680 685

Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn  
690 695 700

Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys  
705 710 715 720

Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His  
725 730 735

Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe  
740 745 750

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys  
755 760 765

Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu  
770 775 780

Gly Leu  
785

<210> 17  
<211> 762  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mature N-terminal IL11-albumin fusion

<400> 17  
Gly Pro Pro Pro Gly Pro Pro Arg Val Ser Pro Asp Pro Arg Ala Glu  
1 5 10 15

Leu Asp Ser Thr Val Leu Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg  
20 25 30

Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe Pro Ala Asp Gly Asp His  
35 40 45

Asn Leu Asp Ser Leu Pro Thr Leu Ala Met Ser Ala Gly Ala Leu Gly  
50 55 60

Ala Leu Gln Leu Pro Gly Val Leu Thr Arg Leu Arg Ala Asp Leu Leu  
65 70 75 80

Ser Tyr Leu Arg His Val Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser  
85 90 95

Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp  
100 105 110

Arg Leu Leu Arg Arg Leu Gln Leu Leu Met Ser Arg Leu Ala Leu Pro  
115 120 125

Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro Leu Ala Pro Pro Ser Ser  
130 135 140

Ala Trp Gly Gly Ile Arg Ala Ala His Ala Ile Leu Gly Gly Leu His  
145 150 155 160

Leu Thr Leu Asp Trp Ala Val Arg Gly Leu Leu Leu Lys Thr Arg  
165 170 175

Leu Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly  
180 185 190

Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu  
195 200 205

Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr  
210 215 220

Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp  
225 230 235 240

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr  
245 250 255

Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu  
260 265 270

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn  
275 280 285

Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe  
290 295 300

His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala  
305 310 315 320

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys  
325 330 335

Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala  
340 345 350

Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala  
355 360 365

Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly  
370 375 380

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe  
385 390 395 400

Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr  
405 410 415

Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp  
420 425 430

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile  
435 440 445

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser  
450 455 460

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro  
465 470 475 480

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr  
485 490 495

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala  
500 505 510

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys  
515 520 525

Thr Tyr Glu Thr Thr Leu Glu Lys Cys